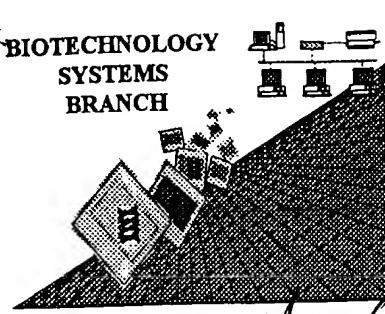


A. Wang

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



Applicant

*AA 6
ACW*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/978,635

Art Unit / Team No.: 1635

Date Processed by STIC: 8/18/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

- 7.

Other: _____

Applicant must provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 0/973,635

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | |
|--|---|
| <input type="checkbox"/> 1 Wrapped Nucleic | <p>The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".</p> |
| <input type="checkbox"/> 2 Wrapped Aminos | <p>The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".</p> |
| <input checked="" type="checkbox"/> 3 Incorrect Line Length | <p>The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.</p> |
| <input type="checkbox"/> 4 Misaligned Amino Acid Numbering | <p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.</p> |
| <input type="checkbox"/> 5 Non-ASCII | <p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p> |
| <input type="checkbox"/> 6 Variable Length | <p>Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.</p> |
| <input type="checkbox"/> 7 Wrong Designation | <p>Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)</p> |
| <input type="checkbox"/> 8 Skipped Sequences (OLD RULES) | <p>Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).</p> |
| <input type="checkbox"/> 9 Skipped Sequences (NEW RULES) | <p>Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000</p> |
| <input type="checkbox"/> 10 Use of N's or Xaa's (NEW RULES) | <p>Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.</p> |
| <input type="checkbox"/> 11 Use of <213>Organism (NEW RULES) | <p>Sequence(s) _____ are missing this mandatory field or its response.</p> |
| <input type="checkbox"/> 12 Use of <220>Feature (NEW RULES) | <p>Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)</p> |
| <input type="checkbox"/> 13 Wrong Format | <p>File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.</p> |

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/978,635DATE: 08/20/98
TIME: 15:26:08

INPUT SET: S28157.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: ELAZAR RABBANI
6 JANNIS G. STAVRIANOPoulos
7 JAMES J. DONEGAN
8 DAKAI LIU
9 NORMAN E. KELKER
10 DEAN L. ENGELHARDT
11 (ii) TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING COMPOSIT
12
13 --> 14 (iii) NUMBER OF SEQUENCES: ~~(42)~~ *delete - per sec 42* *See item 3*
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: ENZO THERAPEUTICS, INC.
18 (B) STREET: C/O ENZO BIOCHEM, INC.
19 527 MADISON AVENUE, 9TH FLOOR
20 (C) CITY: NEW YORK
21 (D) STATE: NY
22 (E) COUNTRY: USA
23 (F) ZIP: 10022
24
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: 3.5" Micro Floppy Disk. 1.44 KB
27 STORAGE
28 (B) COMPUTER: IBM PC/XT/AT, IBM PS/2 OR COMPATIBLES
29 (C) OPERATING SYSTEM: PC-DOS
30 (D) SOFTWARE: MICROSOFT WORD - ASCII TEXT (DOS)
31
32 (vi) CURRENT APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 08/978,635
34 (B) FILING DATE: 25-NOVEMBER-1997
35 --> (C) CLASSIFICATION: Not Yet Known
36
37 (vii) ATTORNEY/AGENT INFORMATION *see item 35*
38 (A) NAME: FEDUS, RONALD C.
39 (B) REGISTRATION NUMBER: 32,567
40 (C) REFERENCE/DOCKET NUMBER: ENZ-53(D4)
41
42 (viii) TELECOMMUNICATION INFORMATION *see item 35*
43 (A) TELEPHONE: (212) 583-0100
44 (B) TELEFAX: (212) 583-0150
45

Printed on 08/20/98 at 15:26:08

more straightforward

or Error summary sheet

Please adjust line spacing globally

Re: Segmentation

or by 72 characters

per line aligned

Fix margins

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/978,635**

DATE: 08/20/98
TIME: 15:26:09

--> 46 (ix)SEQUENCE DESCRIPTION:SEQ ID NO:1:
47

INPUT SET: S28157.raw

delete

(See 1322 h)
Per segment Rebs., and one
spur between or ~~and~~ each

ERRORED SEQUENCES FOLLOW:

-->

48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 20 amino acids
52 (B) TYPE: amino acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: peptide
57
58 (iii) HYPOTHETICAL: NO
59 (X1) <-- first glycine
60 (X2) SEQUENCE DESCRIPTION: SEQ ID
61
62 Gly Phe Phe Gly Ala I
63 x1 S
64
65 Met Ile Ala Gly
66 20 20
67
68

1:
only 18 visible on page

Tip: Anzahl Meisterkästen.
Do NOT use TTB codes between
Anzahl numbers. Use space characters.

Do NOT use TAB codes between
rows numbers. Use spaces instead.

813 (2) INFORMATION FOR SEQ ID NO:42:

814 JOURNAL OF CLIMATE

--> 815 (i) SEQUENCE CHARACTERISTICS
816 (A) LENGTH: 67 base pairs
817 (B) TYPE: nucleic acid
818 (C) STRANDEDNESS: single
819 (D) TOPOLOGY: linear

820 (ii) MOLECULE TYPE: other nucleic acid
821 (A) DESCRIPTION: /desc = "oligonucleotide"

823
824 (iii) HYPOTHETICAL: YES

825 (X) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

827

828 CCGGATAATA CGACTCACTA TAGGGCGAGC TCGGTACCCS GCTCTTAACTT

829 PROTEST 67

830 GCATGCT 87
831

832

833

834

835

60

1st and 2nd

PAGE: 3

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/978,635**

DATE: 08/20/98
TIME: 15:26:10

INPUT SET: S28157.raw

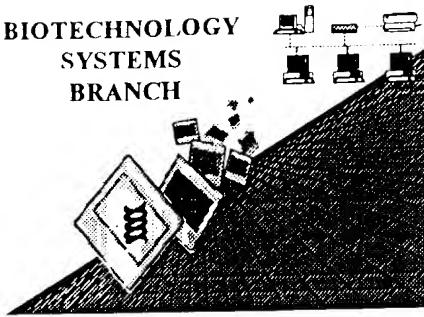
--> 836 LC/WORD/USPROSECUTION/ENZ53D4/SEQUENCE LISTING.060898..enz-53(D4)
837 SEQ ID: PAGE 15
838
839 ENZ-53(D4)
840
841 ENZ-53(D4)
842
843
844

delete

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/978,635**DATE: 08/20/98
TIME: 15:26:10*INPUT SET: S28I57.raw*

Line	Error	Original Text
14	Number of Sequences (0) Doesn't Equal Actual Count (42)	(iii)NUMBER OF SEQUENCES: <u>42</u> --
35	Wrong Classification	(C)CLASSIFICATION:Not Yet Known
46	Unknown or Misplaced Identifier	(ix)SEQUENCE DESCRIPTION:SEQ ID NO:1:
51	Entered (20) and Calc. Seq. Length (19) differ	(A)LENGTH:20 amino acids
816	Entered (67) and Calc. Seq. Length (71) differ	(A)LENGTH:67 base pairs
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	# of Sequences for line conflicts w/ running total	SEQ ID: PAGE 15

BIOTECHNOLOGY
SYSTEMS
BRANCH



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: pub/checker/
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212